

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 100503

TO: Konstantina Katcheves Location: CM1/11C01/11E12

Art Unit: 1636

Friday, August 08, 2003

Case Serial Number: 09/846797

From: Mona Smith

**Location: Biotech-Chem Library** 

CM1-6A01

Phone: 308-3278

mona.smith@uspto.gov

### Search Notes

See attached results.

Thank you for using STIC services
Feel free to contact me if you have any questions.

Mona Smith 308-3278



#### STIC-Biotech/ChemLib

From:

Fredman, Jeffrey

Sent:

Tuesday, August 05, 2003 11:24 AM

To:

STIC-Biotech/ChemLib

Cc:

Katcheves, Konstantina

Subject: FW: RUSH sequence search 09/846797

PLEASE RUSH.

I Approve.

Jeff Fredman

-----Original Message-----

From: Katcheves, Konstantina

Sent: Monday, August 04, 2003 3:26 PM

To: Fredman, Jeffrey

Subject: RUSH sequence search 09/846797

Application serial number: 09/846797

Please search SEQ ID NOs:1 and 6 against the commercial databases only. (29 na and 35 na respectively)

Thank you,

Tina

Konstantina Katcheves

Art Unit 1636

Phone: 305-1999

Office: 11B15 Mailbox: 11E12

2 1/ A

M, SNITH 8/5/05 8/8/03

#### Katcheves, Konstantina

Fr m: Fredman, Jeffrey

S nt: Tuesday, August 05, 2003 11:24 AM

To: STIC-Biotech/ChemLib
Cc: Katcheves, Konstantina

Subject: FW: RUSH sequence search 09/846797

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I Approve.

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Konstantina Katcheves Art Unit 1636

Phone: 305-1999 Office: 11B15 Mailbox: 11E12

#### Katcheves, Konstantina

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Fredman, Jeffrey

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Application serial number: 09/846797

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Thank you, Tina

Konstantina Katcheves Art Unit 1636

Phone: 305-1999 Office: 11B15 Mailbox: 11E12

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Title:
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On Mar 7, 2002 this sequence version replaced g
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 7784
Tel: 979 845 4831
Fax: 979 845 4831
Email: d-ebboletamu.edu
Chromatogram file of this sequence is available
                                                                                                                                                                                                                                                                   mgns011xM14f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgns011xM14 5', mRNA sequence.
BM870744
BM8707442 GI:30404361
                                                                                                                                                                                            Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sor
Sordariomycetes incertae sedis; Magnaporthaceae;
L (bases 1 to 157)
                                                                                                                                        grisea
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3 BQ751733
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BQ4
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  sequence is available,
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AZ931573 AV4. dhz86
AU0014526 PM-BT057-
AI904469 PM-BT057-
AI904469 PM-BT057-
AW792106 D01007-R
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AJ500769 AJ500769
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AJ790444 AU799444
AW791124 D00413-R
CD035900 mgmt011xJ
B0143267 fmh1c.px
B049344 AJ499444
AW791124 D00413-R
CD035900 mgmt011xJ
B0143267 fmh1c.px
B0792634 D01303-F
AZ929878 479. d1156
AZ930332 474. dhz53
B0784402 SnEST4875
B0751736 ESMEED44TF
B0498557 EST07782
B0750940 EST631503
AZ929872 479. d1156
AL420167 T7 end of 56
AL420167 T7 end of 57
CD037449 mgsu011xB
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BR2931163 474. dhz58
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BR2931163 474. dhz59
AZ931163 474. dhz59
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                                                                                                                                                                                                                                                                            Unpublished
Contact: Mitsuoki Morimyo
Genome Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (fission yeast)
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces.
1 (bases 1 to 163)
Morimyo, M. and Mita, K.
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EST.
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Plate: mgns011 row: M
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                                                                                                                                                                                                           National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba. 263-8555, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                pombe
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                                                                                                                                      Anagawa-4-chome, Inage-ku,
l: morimyo@nirs.go.jp.
Location/Qualifiers
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/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
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/mol_type-"mRNA"
/strain-"Guyll"
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/sex="Mat1-2 hermaphrodite"
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Morimyo,M. and Mita,K.
Identification of expressed
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177 bp mRNA linear EST AU010787 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc10371, mRNA sea AU010787
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
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                                                                        Conservative
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Location/Qualifiers
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/note="Vector: Mi3mpl9; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of Mi3mpl9 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
a 37 c 33 g 47 t
                                                                                                                                                             /Glone_lib="Schizosaccharomyces pombe late log phase cDNA"
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Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of wi3mpl9 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
38 c 34 g 55 t 4 others
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/sex="h minus"
                                                                                                                                                                                                                                                                                                                  /clone="spc10371"
/sex="h minus"
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                             /strain-"972"
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                                              Onpublemon Mitsuoki Morimyo
Contact: Mitsuoki Morimyo
Genome Research Group
Genome Institute of Radiological Sciences
National Institute of Radiological Sciences
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AU010656 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc10200, mRNA sequence
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Schizosaccharomyces pombe
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AU010788
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba
Email: morimyo@nirs.go.jp.
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Morimyo, M. and Mita, K.
Identification of expressed
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                  morimyc@nirs.go.jp.
Location/Qualifiers
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/note="Vector: Ml3mp19; The cDNA llbrary of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of Ml3mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
a 42 c 38 g 56 t
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/clone="spc10200"
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tion of expressed
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Genome Research Group
National Institute of Radiological Sciences
National Institute of Radiological Sciences
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Morimyo, M. and Mita, K.
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CTAGTCGGCATAGTTTATGGTTAAGACTACGACGG 102
                                      CTAGTCGGCATAGTTTATGGTTAAGACTACGACGG
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l: morimyo@nirs.go.jp.
Location/Qualifiers
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/note="Yector: M13mp19; The cDNA library of:
Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of M13mp19 DNA and the direction of DN
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
a. 42 c 38 g 56 t
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                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Schizosaccharomyces
/mol_type-"mRNA"
/strain-"972"
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/chone="spc10372"
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Pred. No. 0.00015;
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Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
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National Institute of Radiological Sciences
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AU011658.1 GI:3356567
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AU011658 Schizosaccharomyces
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                                                                                             Morimyo, M. and Mita, K. Identification of expressed
                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe
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AU010835 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc10424, mRNA sequence.
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                                                                                                                                      (bases 1 to 195)
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Location/Qualifiers
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/clone="spc10424"
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/mol_type-"mRNA"
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Pred. No. 0.00015;
Mismatches 0;
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 Similarity
35; Conserv
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba
Email: morinyo@nirs.go.jp
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Morimyo, M. and Mita
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AU011659
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35; Conserv
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Schizosaccharomycetales; Schi:
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/note="Vector: Ml3mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of Ml3mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
a 36 c 43 g 52 t l others
                                                                                      Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of M13mpl9 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)*

36 c 43 g 52 t l others
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                                                                                                                                                                                                   /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
note="Vector: M13mp19; The cDNA library of
                                                                                                                                                                                                                                                          /db_xref="taxon:4896"
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                                                                                                                                                                                                                                                                                                  /strain="972"
                                                                                                                                                                                                                                                                                                               /organism="Schizosaccharomyces pombe"
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/clone="spc11806"
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                   Score 35;
Pred. No.
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Morimyo, M. and Mita, K.
Identification of expressed sequence
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                                  Morimyo, M. and Mita, K.
                                                 Schizosaccharomyces.

1 (bases 1 to 197)
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9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba
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                  Identification of expressed
                                                                                Schizosaccharomycetales; Schizosaccharomycetaceae
                                                                                                 Eukaryota; Fung1; Ascomycota;
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/note="Vector: Mi3mpl9; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of Mi3mpl9 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
a 37 c 45 g 55 t
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/strain-"972"
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/clone="spc01850"
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JOURNAL
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Genome Research Group
National Institute of Radiological Sciences
National Institute of Radiological Sciences
                                                                                                                                                                                                                                                                     Washington University Medical School Box 832, 456 Scott Ave., St. Louis, Tel: 314 362 2735 Fax: 314 362 7855.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ,W.R., Waterston,R.H. and Johnston,M
Surveying Saccharomyces genomes to 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cliften, P.F., Hillier, L.W., Fulton, L., Graves, T., Miner, T.,
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Eukaryota; Fungi; Ascomycota; Saccharo
Saccharomycetales; Saccharomycetaceae;
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AZ931573.1 GI:13502484
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                                                                                                                                                                                                                         Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
                                                                                                                                                                                                                                                                                                                                                                                   Contact: Johnston M
                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                            comparative DNA sequence analysis
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                                                                                                                                                                                                                                                                                                                                                            Department of Genetics
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                                                                                    /organism="Saccharomyces unisporus"
/mol_type="genomic DNA"
/strain="NAREL Y-1556 (CBS 398)"
/db_xref="taxon:27294"
                           /clone_1474.dhz86c05.sl"
/clone_140+"Saccharomyces unisporus
/note="Random genomic sequence
40 c 60 g 57 t
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/strain="972"
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/note="Vector: M13mp19; The cDNA library of
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Score 35; DB 28; Pred. No. 0.00016;

Length 224;

de Souza, S.J. and

Sao Paulo-SP,

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l (bases 1 to 296)

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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Grunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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Schizosaccharomyces pombe (fission yeast)
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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AU007492 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc02102, mRNA sequence.
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PM-BT057-290199-289 BT057
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                   Homo sapiens
                                                                                                                                                                   Homo sapiens (human)
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58 c 44 g 67 t 3 others
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/note="Vector: M13mp19; The cDNA library of
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/mol_type-"mRNA"
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lone="spc02102"
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                                                                                                                                                             Dias Neto,E., Garcia Correa,R., Verjovski-nimerum,V., Costa,F.F., Naggi,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S. Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
             Contact: Simpson A.J.G. Laboratory of Cancer Ge Ludwig Institute for Ca
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 316)
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AI904469
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Ludwig Institute for
Rua Prof. Antonio Pru
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Simpson,A.J.
                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                                                                                               AI904469.1
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=PM&t2-PM-BT057-289.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing
                                                                                                                             sequence tags
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wig Institute for Cancer Research
Prof. Antonio Prudente 109, 4 andar, 01509-010,
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/clone_lib="BT057"
/clone_lib="BT057"
/note="organ: breast; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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/db_xref="taxon:9606"
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                 Research
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Indels

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Gaps

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EST 30-MAR-2000

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BASE COUNT
ORIGIN
Search completed: August 7, 2003, 00:28:29 
Job time: 1896.28 secs
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Best Local Similarity
Matches 35; Conserv
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                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=PM&t2=PM-BT057-389.html
&t3=100299&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
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Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 35; DB 9; inilarity 100.0%; Pred. No. 0.00018; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
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/dev_stage="Adult"
/clone_lib="BT057"
/clone_lib="B
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/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 316;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Minimum
Maximum
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Listing first 45 summaries
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Perfect score:
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1: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:
2: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:
3: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:
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5: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:
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8: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
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Helper oligonucleo
S. arieticanis sma
T. gondii small ri
S. neurona small ri
S. muris small rib
S. capricanis small
S. gigantea small
C. albicans 18S RN
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48711857771666666666666666666666666666666	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
2022224444441964622451	
AAF11316 ABZ80030 ABV78726 ABA01154 ABA01154 ABA01152 ABA01152 ABA01152 ABA01152 ABA01152 ABA01152 ABA01152 ABA01152 ABA01152 ABV78705 ABAV78705 ABV78706 ABV78711 AB	AA170915 AA170916 AA471226 AA471229 AA471230 AA471228 AA471227 AA471227 AA471227 AA471231 AA471231 AA751946
Aspergillus niger Xylariales filamen C. sinensis rRNA s Bulgaria Inquinans Deuteromycetes pol. A. fumigatus 18S r Deuteromycetes pol. Bovine Neospora s Neospora nuclear s Neospora nuclear s Neospora nuclear s Neospora nuclear s Neospora ss-rRNA C. crassispora rRNA C. crassispora rRNA C. sinensis rRNA s C. sinensis r	Candida species 18 Candida species 18 C krusei 165 rRNA C tropicalis 165 C albicans 165 rR C parapsilosis 16 T glabrata 165 rR A fundgatus 165 rA A fundgatus 165 rA A spergillus oryzac Cordyceps sinensis Sequence surroundi 185 rRNA gene. Pn

# ALIGNMENTS

12-MAR-2002 (first entry)

Helper oligonucleotide CalA1005 for Candida spp. detection

AAI70914 standard; DNA;

35 ₽P

AAI70914;

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RRESULT 1
ARAT70917
ANA 770917
XX AAIT70917
XX AAIT70917
XX AAIT7
XX AAIT7
XX CANC
XX 
Novel oligonucleotide sequences that are fully complementary to ribosomal RNA or DNA of Candida species, useful for detecting presence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans; Candida tropicalis; Candida dubliniensis; Candida viswanathii; Candida parapsilosis; detection; ss.
                                                                                                                                                                          WPI; 2002-066537/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000; 2000US-201249P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2001; 2001WO-US13884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                          (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                          Gordon PC;
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
   1470-1487 of the small ribosomal subunit of Sarcocystis ne primer is unique to the S. neurona species. The primer is diagnostic tests for Equine protozoal myeloencephalitis (El the presence of S. neurona is indicative of EPM. To find a sequence unique to S. neurona small ribosomal suburona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida viswanathii and Candida tropicalis. Probe CalA1038 can distinguish these Candida species from their known phylogenetically nearest neighbours, and is useful for their detection and quantitation. The Tm of interaction between probe and C. albicans risk increased from 57.8 to 62.2 degrees C when the helper risk increased from 57.8 to 62.2 degrees C when the helper
                                                                                                             Sarcocystis neurona diagnostic primer, useful for in vitro diagnostic testing for Equine protozoal myeloencephalitis, i.e. for diagnosing tipresence of S. neurona in equine blood or cerebrospinal fluid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligonucleotide was added to the hybridisation reaction, and increased to 63.2 degrees C when another helper oligonucleotide, CalAi066 (see AAi70912), was also included.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of helper oligonucleotide CalA1006, which binds target Candida spp. ribosomal RNA molecules at a site immediately adjacent to probe CalA1038 (see AA170913). The helper oligonucleotide promotes the highly specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hybridisation of CalA1038 probe to a sequence found in the 18s of Candida albicans, Candida tropicalis, Candida dubliniensis, Candida viswanathii and Candida tropicalis. Probe CalA1038 ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of.
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35; Conserv
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                                                                                                                                                                                                         KENTUCKY RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.dubliniensis,
                                                                                                                                                                                                                                                                                                                                                                              small ribosomal subunit nucleotide sequence fragment
                                                                                                                                                                                                                               9505-0388029
                                                                                                                                                                                                                                                     9505-0388029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; 6 C; 10 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                         SRSU;
  gigantea,
                                                                                                                                                                                   Dubey JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.viswanathii, C.parapsilosis
                                                                                                                                                                                                                                                                                                                                                         Equine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
             ribosomal subunit sequences
                                                                                                                                                                                   Granstrom
                                                                                                                                                                                                                                                                                                                                                        protozoal
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  capicanis,
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                                                          neurona.
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                                   (EPM)
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eurona. This
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RESULT 3
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Best Local
                                                        Matches
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                                                                                                                                                    The present invention relates to a diagnostic primer from positions 1470-1487 of the small ribosomal subunit of Sarcocystis neurona. This primer is unique to the S. neurona species. The primer is useful for diagnostic tests for Egyline protozoal myeloencephalitis (EPM) where the presence of S. neurona is indicative of EPM. To find a sequence unique to S. neurona small ribosomal subunit sequences from S. neurona, S. muris, S. gigantea, T. gondii, S. capicanis, S. arieticanis, S. cruzi, S. tenella, E.tenella and C. parvum were compared. The present sequence is a fragment of the small ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA94985
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                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                 Fenger
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                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                               presence
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                                                                                                                                                                                                                                                                                                                                                           Sarcocystis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-1995;
                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gondii.
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                                                                      Similarity
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CTAGTCGGCATAGTTTATGGTTAAGACTACGACGG
                                                     100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                B₽;
                                                                                                                                                                                                                                                                                                                            neurona diagnostic primer, useful for in vitro diagnostic Equine protozoal myeloencephalitis, i.e. for diagnosing t S. neurona in equine blood or cerebrospinal fluid -
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                                                                                                                                                                                                                                                                                                 Fig 1; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gajadhar AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cruzi, S. tenella,
                                                                                                                                            this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunit;
                                                                                                              A; 12 C; 11 G; 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; 12 C; 11 G; 11 T;
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Pred. No.
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                                                                      Pred.
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                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   Granstrom
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                                                                                                              0 other;
                                                                      4.6e-06;
                                                                                   DB
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small ribosomal
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AAA94978/c
ID AAA94978 standard; DNA; 52
XX
AC AAA94978;
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AC AAA94978;
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IO-JAN-2001 (first entry)
XX
S. neurona small ribosomal
XX
Small ribosomal subunit; {
KW EPM; diagnosis; ds.
XX
OS
S. neurona.
PN US6110665-A.
PN US6110665-A.
PN US6110665-A.
PP 14-FEB-1995; 95US-03880
XX
PF 14-FEB-1995; 95US-03880
XX
CENT ) UNIV KENTUCKY RES
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PT 5-AUG-2000
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PF 14-FEB-1995; 95US-03880
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RESULT 5
AAA94979/
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic tests for Equine protozoal myeloencephalitis (Eppthe presence of S. neurona is indicative of EpM. To find a sequence unique to S. neurona small ribosomal subunit sequence. S. neurona, S. muris, S. gigantea, T. gondii, S. capicanis, arieticanis, S. cruzi, S. tenella, E. tenella and C. parvum compared. The present sequence is a fragment of the small risubunit used in this comparison.
                                                                                                                                                                                                                                                                                                            S. muris small ribosomal subunit nucleotide sequence fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a diagnostic primer 1470-1487 of the small ribosomal subunit of Sarcocyst
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                                        US6110665-A
                                                                                                                     S. muris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA94979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA94979 standard; DNA;
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                                                                                                                                                                                                                                           Small
                                                                                                                                                                                              l ribosomal
diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                              subunit;
ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ntion relates to a diagnostic primer from positions small ribosomal subunit of Sarcocystis neurona. This to the S. neurona species. The primer is useful for for Equine protozoal myeloencephalitis (EPM) where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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Pred. No. 4.7
); Mismatches
                                                                                                                                                                                                                                   Equine protozoal myeloencephalitis;
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. 4.7e-06;
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RESULT 6
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ID AAA94980
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Best Local S
Matches 35
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testing for
presence of
                                                                                                                                                                                    US6110665-A
                                                                                                                                                                                                        capricanis
                                                                                                                                                                                                                                         Small ribosomal
                                                                                                                                                                                                                                                            S. capricanis small ribosomal subunit nucleotide sequence fragment
                                                                                                                                                                                                                                                                                    10-JAN-2001
                                                                                                                                                                                                                                                                                                          AAA94980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence unique to S. neurona small ribosomal subunit sequences S. neurona, S. muris, S. gigantea, T. gondii, S. capicanis, S. arieticanis, S. cruzi, S. tenella, E.tenella and C. parvum were compared. The present sequence is a fragment of the small ribosompared.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer is unique to the S. neurona species. The primer is useful for diagnostic tests for Equine protozoal myeloencephalitis (EPM) where the presence of S. neurona is indicative of EPM. To find a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a diagnostic primer from positions 1470 \cdot 1487 of the small ribosomal subunit of Sarcocystis neurona. The
                                                                                                                    14-FEB-1995;
                                                                                                                                          14-FEB-1995;
                                                                                                                                                               29-AUG-2000.
                                                                                                                                                                                                                              EPM; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subunit used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
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                                                                                               (KENT ) UNIV KENTUCKY RES FOUND
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                                                                         CK,
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35; Conserv
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                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                CTAGTCGGCATAGTTTATGGTTAAGACTACGACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurona diagnostic primer, useful for in vitro diagnostic Equine protozoal myeloencephalitis, i.e. for diagnosing the S. neurona in equine blood or cerebrospinal fluid.
                                                                         Gajadhar
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
llarity 100.0%;
Conservative
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                                                                                                                    9505-0388029
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                                                                                                                                                                                                                                                                                                                              DNA;
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                                                                                                                                                                                                                                                                                   entry)
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                                                                         Dubey
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB
Pred. No. 4.7
D; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 T;
                                                                         Granstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Granstrom
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4.7e-06;
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Sarcocystis neurona diagnostic primer, useful for in vitro diagnostic testing for Equine protozoal myeloencephalitis, i.e. for diagnosing the presence of S. neurona in equine blood or cerebrospinal fluid -

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RESULT 7
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ID AAA949
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XX AAA949
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XW EPM; d
XX Small
KW EPM; d
XX S. 919
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Best Local
                                           1470-1487 of the small ribosomal subunit of Sarcocystis neurona. This primer is unique to the S. neurona species. The primer is useful for diagnostic tests for Equine protozoal myeloencephalitis (EPM) where the presence of S. neurona is indicative of EPM. To find a sequence unique to S. neurona small ribosomal subunit sequences from S. neurona, S. muris, S. glyantea, T. gondil, S. capicanis, S. arieticanis, S. cruzi, S. tenella, E. tenella and C. parvum were compared. The present sequence is a fragment of the small ribosomal subunit used in this comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sarcocystis
testing for
presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a diagnostic primer from positions 1470-1487 of the small ribosomal subunit of Sarcocystis neurona. This primer is unique to the S. neurona species. The primer is useful for diagnostic tests for Equine protozoal myeloencephalitis (EPM) where the presence of S. neurona is indicative of EPM. To find a sequence unique to S. neurona is indicative of EPM. To find a sequence unique to S. neurona small ribosomal subunit sequences from S. neurona, S. muris, S. gigantea, T. gondil, S. capicanis, S. arieticanis, S. cruzi, S. tenella, E.tenella and C. parvum were compared. The present sequence is a fragment of the small ribosomal subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. gigantea
                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
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     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Small ribosomal EPM; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2001
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  ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                    neurona diagnostic primer, useful for in vitro diagnostic Equine protozoal myeloencephalitis, i.e. for diagnosing to S. neurona in equine blood or cerebrospinal fluid -
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                                                                                                                                                                                                                                                                                                                                                               Fig 1; 41pp;
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  12 C;
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                                                                                                                                                                                                                                                                                                                                                               English.
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     11 G;
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4.7e-06;
hes 0;
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Query

Match

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Length

RESULT 9
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ID AAI7
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(first entry)

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RESULT 8
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                                                                     Query Match
Best Local
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                                                                                                                                                               This invention describes a novel multiplex amplification reaction for detecting clinically relevant fungal infections by amplifying a region the 18s RNA gene, where only sequences from pathogenic Candida and Aspergillus species are amplified. The method is quick, simple and sensitive, and can detect all clinically important Candida and Aspergillus species, but generally it does not detect species commonly present in laboratories as contaminants (avoiding false positive results). The detection limit is 3-20 cells/10 ml of blood, depending the detection method and makes as contaminants.
                                                                                                                                                                                                                                                                                                                               Multiplex amplification for detecting fungal clinically important strains of Candida and amplifying a region of the 18S RNA gene -
                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-2002
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                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                    Claim 13; Page 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2000; 2000DE-1048009
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                                                                                                                                          detection
method of
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EC
            CTAGTCGGCATAGTTTATGGTTAAGACTACGACGG 35
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CTAGTCGGCATAGTTTATGGTTAAGACTACGACGG
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                                                                                                               BP;
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                                                       Conservative
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                                                                                                                                          method used. This sequence represents the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathogenic;
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                                                                                                               A; 20 C; 14 G;
                                                                                                                                                                                                                                                                                                    27pp; German
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                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Kirschner
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da and Aspergillus,
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thes 0;
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RESULT 10
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ID AAI709
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                              Candida
Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligonuclectides (see AAI70909-14) correspond to a portion of this sequence or its complement. The probes are highly specific, and can distinguish these Candida species from their known phylogenetically nearest neighbours. They are useful for detection and quantitation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Candida
Candida
                                                                                                                                                                                                                                                                                                                                                             Candida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of DNA corresponding to a unique segment (see AAI70916) of the 18S ribosomal RNA of Candida albicans, Candida tropicalis, Candida dubliniensis, Candida viswanathii and Candida tropicalis. Claimed hybridisation probes and helper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribosomal of C.albi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel oligonucleotide sequences that are fully complementary to ribosomal RNA or DNA of Candida species, useful for detecting presence of Calbicans, C.dubliniensis, C.viswanathii, C.parapsilosis in test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2001;
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                         (GENP-) GEN-PROBE INC
                                                                   01-MAY-2000; 2000US-201249P
                                                                                                               01-MAY-2001;
                                                                                                                                                             08-NOV-2001
                                                                                                                                                                                                      WO200183821-A2
                                                                                                                                                                                                                                                  Candida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI70916;
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                                                                                                                                                                                                                                                albicans
                                                                                                                                                                                                                                                                                            albicans; Candida tropicalis; viswanathii; Candida parapsilo
                                                                                                                                                                                                                                                                                                                                                          species 18S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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llarity 100.0%;
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ida parapsilosis; detection; probe; ss.
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                                                                                                                                                                                                                                                                                          parapsilosis;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                             RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 T; 0 other;
                                                                                                                                                                                                                                                                                                                 Candida dubliniensis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.2e-06;
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                                                                                                                                                                                                                                                                                       detection; probe;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel oligonucleotide sequences that are fully complementary in ribosomal RNA or DNA of Candida species, useful for detecting of C.albicans, C.dubliniensis, C.viswanathii, C.parapsilosis:
                                                                           diagnosing bacterial infections, by hybridization with oligonucleotides
                                                                                                                                                                                                                                                                                                                                             food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of a unique segment of th ribosomal RNA of Candida albicans, Candida tropicalis, Candida dubliniensis, Candida viswanathii and Candida
                                                                                       Rapid determination of microbial nucleic acid, useful e.g. for diagnosing bacterial infections, by analysis of temperature-dependent
                                                                                                                                              Hoeft A,
                                                                                                                                                                    (HOEF/)
                                                                                                                                                                                                                                                                                                           Candida krusei.
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                                                       Disclosure;
                                                                                                                         WPI; 2001-425677/45.
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31-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                 detection; ss
                                                                                                                                                                                                                                                                                                                                                       Hybridization;
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                                                                                                                                                                                                                                                                                                                                          monitoring;
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                                                                                                                                                                      HOEFT A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA; 421
                                                                                                                                              Stueber F;
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                                                      Figure
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP;
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                                                                                                                                                                                                                                                                                                                                                                              rRNA DNA fragment YSASRSUD
                                                                                                                                                                                                                                                                                                                                         diagnosis; bacterial infection;
g; water monitoring; veterinary;
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                                                       German.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                         sepsis; fungal infection;
forensic; primer; probe;
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in test
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This invention describes a novel method for detecting microbial DNA/RNA (I) by concentrating (I) from a sample, adding at least one labeled oligonucleotide (ON), performing temperature-dependent hybridization and determining (I) from the physical properties of the (I)-ON complex, e.g

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RESULT 12
AAH21229;
AAH21229;
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AAH21229;
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AAH21229;
XX
DT 13-SEP-2001 (first entry)
DT 13-SEP-2001 (first entry)
DE C. tropicalis 16S rRNA DNA fra
XX
Hybridization; diagnosis; baci
KW food monitoring; water monitol
KW detection; ss.

OS Candida tropicalis.

YX
W0200148237-A2.

YX
W0200148237-A2.

PD 05-JUL-2001.

XX
W7
PD 05-JUL-2001.

XX
AN W0200148237-A2.

PR 23-DEC-1999; 99DE-1062895.
PR 23-DEC-1999; 99DE-1062895.
PR 31-MAY-2000; 2000MO-DE04610.

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HOEF/) HOEFT A.
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Best Local
   This invention describes a novel method for detecting microbial DNA/RNA (I) by concentrating (I) from a sample, adding at least one labeled olligonucleotide (ON), performing temperature-dependent hybridization and determining (I) from the physical properties of the (I)-ON complex, e.g. the temperature dependence of hybridization. The method is used for rapid determination of microbial genomic RNA or DNA, particularly for diagnosis of bacterial infections (e.g. sepsis) or fungal infections (particularly in intensive care patients), also for monitoring food and water, and for veterinary or forensic investigations. The method provides quick (typically less than 3 hours) quantitative and qualitative determination/identification of microbial nucleic acid. It is very sensitive, allowing early diagnosis of infection. ARRIGIG-ARHZ1231 represent primers and probes used to illustrate the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rapid determination of microbial nucleic acid, useful e.g. for diagnosing bacterial infections, by analysis of temperature-dependent hybridization with oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hybridization; dlagnosis; bacterial infection;
food monitoring; water monitoring; veterinary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. tropicalis 16S rRNA DNA fragment YSASRSUG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Figure 13; 57pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 CTAGTCGGCATAGTTTATGGTTAAGACTACGACGG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \mathbf{L}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
6.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
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forensic; primer; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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CTAGTCGGCATAGTTTATGGTTAAGACTACGACGG

Matches Query Match Best Local

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100.0%; ilarity 100.0%; Conservative (

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Score 35; DB Pred. No. 6.3

6.3e-06;

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DB

22;

Length Indels

Sequence 431

BP; 115

A; 86 C;

110 G; 120

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RESULT 13
AAH21230/c
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Best Local
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                              This invention describes a novel method for detecting microbial DNA/RNA (I) by concentrating (I) from a sample, adding at least one labeled oligonucleotide (ON), performing temperature-dependent hybridization and determining (I) from the physical properties of the (I)-ON complex, e.g. the temperature dependence of hybridization. The method is used for rapid determination of microbial genomic RNA or DNA, particularly for diagnosis of bacterial infections (e.g. sepsis) or fungal infections (particularly in intensive care patients), also for monitoring food and water, and for veterinary or forensic investigations. The method provides quick (typically less than 3 hours) quantitative and qualitative determination/identification of microbial nucleic acid. It is very sensitive, allowing early diagnosis of infection. AAH21160-AAH21231 represent primers and probes used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. albicans
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                                                                                                                                                                                                               Disclosure; Figure 13; 57pp; German.
                                                                                                                                                                                                                                                       Rapid determination of microbial nucleic diagnosing bacterial infections, by analy
                                                                                                                                                                                                                                                                                                                                             (HOEF/)
                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999; 99DE-1062895.
31-MAY-2000; 2000DE-1027113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hybridization; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH21230
                                                                                                                                                                                                                                          hybridization with oligonucleotides
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                                                                                                                                                                                                                                                                                                                     Hoeft A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     food monitoring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380
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                                                                                                                                                                                                                                                                                                                                             ) HOEFT A.
) STUEBER F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                     Stueber F;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      water monitoring; veterinary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
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                                                                                                                                                                                                                                                      cleic acid, useful e.g. for
analysis of temperature-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sepsis; fungal infection;
forensic; primer; probe;
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RESULT 15
AAH21227/c
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AAH21228/C
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                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                        This invention describes a novel method for detecting microbial DNA/RNA (I) by concentrating (I) from a sample, adding at least one labeled oligonucleotide (ON), performing temperature-dependent hybridization and determining (I) from the physical properties of the (I)-ON complex, e.g. the temperature dependence of hybridization. The method is used for rapid determination of microbial genomic RNA or DNA, particularly for diagnosis of bacterial infections (e.g. sepsis) or fungal infections (particularly in intensive care patients), also for monitoring food and water, and for veterinary or forensic investigations. The method provides quick (typically less than 3 hours) quantitative and qualitative determination/identification of microbial nucleic acid. It is very sensitive, allowing early diagnosis of infection, AH21160-AAH21231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOEF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rapid determination of microbial nucleic acid, useful e.g. for diagnosing bacterial infections, by analysis of temperature-dependent hybridization with oligonucleotides
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 AAH21227;
                              .227/c
AAH21227 standard;
                                                                                                                                                                                                                   Sequence 432 BP;
                                                                                                                                                                                                                                                               represent primers and probes used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Figure 13; 57pp; German.
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31-MAY-2000; 2000DE-1027113.
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                                                                                                                                                                            Local
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monitoring; water monitoring; veterinary; forensic; primer; probe;
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STUEBER F.
                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stueber F;
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llarity 100.0%;
Conservative
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                               DNA; 444 BP
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Pred. No.
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                                                                                                                                                                         6.3e-06;
                                                                                                                                                                                          DB
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                                                                                                                                                                                                                                                                                                                                                                                                     Rapid determination of microbial nucleic acid, useful e.g. for diagnosing bacterial infections, by analysis of temperature-dependent hybridization with oligonucleotides \,
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31-MAY-2000;
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food monitoring; water monitoring; veterinary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T. glabrata 16S rRNA DNA fragment YSLSRSUA
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Figure 13; 57pp; German.
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395
                                                         35;
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STUEBER F.
                                                                         Similarity
              CTAGTCGGCATAGTTTATGGTTAAGACTACGACGG
                                                                                                                   444
CTAGTCGGCATAGTTTATGGTTAAGACTACGACGG
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                                                        100.0%; ilarity 100.0%; Conservative
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2000DE-1027113
                                                                                                                     ВP;
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                                                                                                                     115
                                                                                                                   A; 89 C;
                                                         0,
                                                        Score 35; DB 22;
Pred. No. 6.3e-06;
; Mismatches 0;
                                                                                                                     117 G;
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Title:
Perfect score:
Sequence:

US-09-846-797-6 35 1 ctagtcggcatagtttatggttaagactacgacgg 35 OM nucleic - Run on:

nucleic search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

August 6, 2003, 21:26:11; Search time 856.953 Seconds (without alignments) 1670.846 Million cell updates/sec

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: \*

gb\_ba:\*
gb\_htg:\*
gb\_in:\*

gb\_om:\*

gb\_pat: gb\_ph: gb\_pl: gb\_pr: gb\_pr: gb\_ro: gb\_sts: gb\_sy: Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

5777422

2888711 seqs, 20454813386 residues

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Pred. No. is the number of results predicted by chance to have a
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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and Dubey, J.P

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Renger,C.K., Granstrom,D.E., Gajadhar,A.A. and Du

Sarcocystis neuronadiagnostic primer and its use
equine protozoal myeloencephalitis diagnosis

Patent: US 6110665-A 81 29-AUG-2000;

Location/Qualifiers
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 l Similarity
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Fenger, C.K., Granstrom, D.E., Gajadhar, A.A. and Dubey, J.P.
Sarcocystis neuronadiagnostic primer and its use in methods of
equine protozoal myeloencephalitis diagnosis
Patent: US 6110665-A 85 29-AUG-2000;
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/mol_type="genomic DNA"
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Fenger, C.K., Granstrom, D.E., Gajadhar, A.A. and Du Sarcocystis neuronadiagnostic primer and its use equine protozoal myeloencephalitis diagnosis patent: US 6110665-A 79 29-AUG-2000;
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Lanspora coronata

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordario

Rypooreomycetidae; Halosphaeriales; Halosphaeriaceae;

1 to 72)

Spatafora,J.W., Volkmann-Kohlmeyer,B. and Kohlmeyer,J

**The Amendant terrestrial origins of the Halosphaeriale;
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  2 (bases 1 to 72)
Spatafora, J.W., Vo
Direct Submission
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Fenger, C.K., Granstrom, D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
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AR107730
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Fenger, C.K., Granstrom, D.E., Gajadhar, A.A. an Sarcocystis neuronadiagnostic primer and its equine protozoal myeloencephalitis diagnosis Patent: US 6110665-A 80 29-AUG-2000;
                                                                                                                Lanspora coronata
                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.
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           Volkmann-Kohlmeyer, B.
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           and Kohlmeyer, J
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Candida albicans
Candida albicans
Eukaryota: Fungi; Ascomycota;
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Sequence 6
AX406742
                                                                                                         Sequence 7
AX298065
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                            AX298065.1
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                                                                                                                                                                                                                                                                                                                                                                /organism="Candida albicans"
/mol_type="genomic DNA"
/mol_xref="taxon:5476"
/db_xref="taxon:5476"
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/strain="JK 4839A"
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 CAZ81374

C. BETUGINOSA 185 TRNA GENE.

Z81374

Z81374.1 GI:2808818

185 TIDOSOMAI RNA; 185 TRNA GENE.
Chlorociboria aeruginosa
Chlorociboria aeruginosa
Chlorociboria aeruginosa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Helotiaceae; Chlorociboria.
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Candida albicans
Eukaryota; Fungi; Ascomycota;
Eukaryota; mitosporic
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Patent: WO 0183821-A 7
Gen-Probe Incorporated
Holst-Jensen, A
                                                                                                                                                                                                                                                                                                                                                                              Patent: WO 0183821-A 8 08-NOV-2001; Gen-Probe Incorporated (US)
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/mol_type="mRNA"
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/mol_type="genomic DNA"
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Location/Qualifiers
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from Patent WO0183821.
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                       uncultured saccharomycete uncultured saccharomycete
                                                                X91535.1 GI:987810
18S ribosomal RNA; 18S rRNA
                                                                                                                    Uncultured saccharomycete X91535
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Sarcocystis gigantea
Eukaryota; Alveolata; Apicomplexa;
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    Eukaryota;
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Submitted (29-OCT-1996) Holst-Jensen
Department of Biology, University of
0316, Oslo, NORWAY
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llarity 100.0%;
Conservative (
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26 c 34 g 36 t
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/mol_type="genomic DNA"
/strain="1785.P on dead hardwood"
/db_xref="taxon:54693"
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36 c 39 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sarcocystis
/mol_type="rRNA"
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RESULT 15
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AUTHORS
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Tenter,A.M., Baverstock,P.R. and Johnson,A.M.
Tenter,A.M., Baverstock,P.R. and Johnson,A.M.
Phylogenetic relationships of Sarcocystis species from sheep, goats, cattle and mice based on ribosomal RNA sequences int. J. Parasitol. 22 (4), 503-513 (1992)
                                                                                                                                                                                                                                                                                                                                                                                          Sarcocystis capracanis
Sarcocystis capracanis
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                      GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 110244] from the original journal article. This sequence comes from Fig. 1C and 1D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $41710.1 GI:252752
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                                         /organism="Sarcocystis capracanis"
/mol_type="rRNA"
/db_xref="taxon:5816"
/db_xref="taxon:5816"
/order($41720.1:1. .210,join($41716.1:1.
/gene="small subunit rRNA"
order($41720.1:1. .210,join($41716.1:1.
/gene="small subunit rRNA"
            /product="small subunit ribosomal RNA"
43 c 53 g 70 t 18 others
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/environmental_sample
/country="Canada"
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/mol_type="genomic DNA"
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Pred. No. 0.91;
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Search completed: August 6, 2003, 23:29:02 Job time: 858.953 secs

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Contact: Elizabeth H. H.
DCMB Box 91000
Duke University
Durham, NC 27708-1000,
Tel: 919 613 8164
Fax: 919 613 8177
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Eukaryota: Viridiplantae: Chlorophyta: Chlorophyceae; Volvocales;
Eukaryota: Chlamydomonas.
                                                                                                                                                            Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation Vascular Plants; project phase 2
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                    Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefégenoscope.cns.fr - Web : This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
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1 (bases 1 to 943)
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segref@genoscope.cns.fr - Web :
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                                                                                                                                                                                                                           Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.

Wincker,P. and Weissenbach,J.

Sephoration of the heniascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                    Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Souclet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
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                                                                                                                                                                                                                                              FEBS Lett. 487 (1), 91-94 (2000)
                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 949)
Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F.
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                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                        tropicalis
                                                                                                                                                                                                                                                                                           Genomic exploration of the hemiascomycetous yeasts: 16. Candida
                                                                                                                                                                                                                                                                                                                    Dujon,B.
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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/clone="BDOAA003G09"
/clone_lib="BDOAA"
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/strain="CBS 94"
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RESULT 4
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2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segrefégenoscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                                                                           FEBS
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Soucitet, J. L., Algle, M., Artiguenave, F., Blandin, G.,
Soucitet, J. L., Algle, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Duron, Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
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T7 end of clone XBD0AA002C12 of library XBD0AA
of Candida tropicalis, genomic survey sequence.
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                                                                                                                        Submitted (08-SEP-2000) Genoscope - Centre National de
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/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
/clone="BDOAA013C01"
/clone_lib="BDOAA"
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contains 35s rDNA"
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T7 end of clone BD0AA016B05
Candida tropicalis, genomic
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                                                                                                                                                                                                                                            Souciet, J.L., Aiglé, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potler, S.
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of yearst species for molecular evolution studies
                                                                                                                                                                                                                                                                                 Genomic exploration of the hemiascomycetous yeasts: 16. Candida
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Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F.
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                                                       Direct Submission
                                                                                                                                                      Genoscope
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/clone_lib="XBD0AA"
/note="end : T7"
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188 c 249 g 252
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/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
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nic survey sequence.
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CNS07E4J/c
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefégenoscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygoṣaccharomyces rouxii,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Souciet, J.L., Aiglé, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montign, J., Dujon, B., Durens, P., Lepingle, A., Liorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS07E4J 966 bp DNA linear T7 end of clone XBD0AA001A07 of library XBD0AA from of Candida tropicalis, genomic survey sequence.
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Blandin,G.,
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                                                                                                                                    Direct Submission
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20584726
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Saccharomycetales; mitosporic
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29; Conserv
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/mol_type-"genomic DNA"
/strain-"CBS 94"
/db_xref-"taxon:5482"
/clone-"BDOAAO16BO5"
/clone_11b-"BDOAA"
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182 c 256 g 268
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Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F.
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqreff@genoscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                  Genoscope.
Direct Submission
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Wincker, P. and Weissenbach, J.
Yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 971)
Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F.
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de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Liorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
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1 (bases 1 to 971)
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/clone="XBD0AA001A07"
/clone_11b="XBD0AA"
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/mol_type="genomic DNA"
/strain="CBS 94"
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremteux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégénoscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                                                                                         FEBS
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Souciet, J.L., Algle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS07CU3 994 bp DNA linear GSS (T7 end of clone BD0AA006H01 of library BD0AA from strain Candida tropicalis, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                               Genomic exploration of the hemiascomycetous yeasts: 16. Candida
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Candida tropicalis
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                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 994)
Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F.
                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                                                            Dujon, B.
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/clone="BDOAA010H04"
/clone_lib="BDOAA"
/clone_lib="BDOAA"
/note="end: T7"
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188 c 252 g 272 t
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segref@genoscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S., de-Montigny, J., Dulon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.

Wincker, P. and Weissenbach, J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Direct Sul
                                                                                                                                                                                                                               FEBS Lett. 487
20584726
                                                                                                                                                                                                                                                                                           Genomic exploration
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/mol_type="genomic DNA"
/strain="CBS 94"
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                This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail segrefégenoscope.cns.fr - Web :
                                                                                                                                                                                                                                                                                                                                                                                                                                      Souciet, J.I., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S.,
de-Montigny, J., Dulon, B., Durrents, P., Lepingle, A., Llorente, B.
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set Cyeast species for molecular evolution studies
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                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1010)
Blandin,G., Ozler-Kalogeropoulos,O., Wincker,P., Artiguenave,F.
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/clone="BDOAA001H09"
/clone_11b="BDOAA"
/note="end : T7"
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Submitted (Q8-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequencscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var: uvarum, Saccharomyces
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida
                                                                                                                    Direct Submission
                                                                                                                                     Genoscope
                                                                                                                                                                                                                       FEBS Lett. 487 (1), 91-94 (2000)
                                                                                                                                                                                                                                                            Genomic exploration of the hemiascomycetous yeasts: 16. Candida
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Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F.
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FEBS Lett. 487 (1), 3-12 (2000)
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AL441466.1
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/clone="BD0AA006B09"
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/mol_type="genomic
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1 (bases 1 to 1029)

Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S.,
de-Montigny, J., Dulon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potter, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of present species for molecular evolution studies
            Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequencage) cons.fr - Web:
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
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Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F.
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exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
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/clone_11b="XBD0AA"
/note="end : T3"
<1. .>1027
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/mol_type="genomic DNA"
/strain="CBS 94"
/db_xref="taxon:5482"
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequencioscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                    Souciet J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S., de-Montigny, J., Dujon, B., Durens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
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Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                                 Direct Submission
                                                                                                                                  Genoscope
                                                                                                                                                                                                                     FEBS Lett. 487
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/note="end : T7"
<1. .>1029
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/strain="CBS 94"
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/clone="BD0AA013E02"
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exiguus, Saccharomyces servazzii, Zygosaccharomyces

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1 (bases 1 to 1038)

Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Ralogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
         Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefgenoscope.cns.fr. Web :
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
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Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
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                                                                                                                                 Direct Submission
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/clone="BD0AA012F03"
/clone_11b="BD0AA"
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/strain="CBS 94"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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Best Local S
Matches 29
                                                                                                                                                                                                                            JOURNAL MEDLINE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr - Web: This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottler, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, R., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.

Wincker, P. and Weissenbach, J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida tropicalis
Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                            Genoscope.
                                                                                                                                                                                                                                                                                     Genomic exploration of the hemiascomycetous yeasts: 16. Candida
                                                                                                                                                                                                                                                                                                                               2 (bases 1
Blandin,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO7CNA 1041 bp DNA linear GSS (T3 end of clone BDOAA004C06 of library BDOAA from strain Candida tropicalis, genomic survey sequence.
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29; Conserv
                                                                                                                                          Direct Submission
                                                                                                                                                                                                                            20584726
                                                                                                                                                                                                                                                FEBS Lett. 487
                                                                                                                                                                                                                                                                      tropicalis
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AL439388.1 GI:12222801
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265 c 197 g 291 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="end : <1. .>1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:5482"
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/clone_11b="BDOAA"
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Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
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Lrain CBS 94 of
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BASE COUNT
ORIGIN
Search completed: August 7, 2003, 00:28:26 Job time: 1570.72 secs
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                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                        Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                 287 a
                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Candida tropicalis"
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/strain-"CBS 94"
/db_xref-"taxon:5402"
/clone-"BDDAA004C66"
/clone-"BDDAA0 4C66"
/clone-11b-"BDDAA"
/note-"end: T3"
                                                                                                                                                                                                                                                                                                          /note="part of rDNA repeats
contains 35S rDNA"
/evidence=not_experimental
a 272 c 198 g 282 t
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 200000000
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Match
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Gapop 10.0 , Gapext 1.0
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.Published_Applications_NA:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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'cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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 US-10-027-632-314242

US-10-265-689-25

US-09-764-891-8197

US-10-027-632-99343

US-10-027-632-903956
                                                                                                                                    US-10-027-632-46818
US-10-027-632-46819
US-10-027-632-77880
US-10-027-632-77881
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US-09-938-842A-5257
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                                                                                                                       10-027-632-314241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /pubpna/US09B_PUBCOMB.seq:*
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8197, Ap
89343, A
303956,
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46818, A
46819, A
77880, A
77881, A
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5257, A
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## ALIGNMENTS

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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-288539
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Matches 21
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SEQ ID NO 288539
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR EILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                       LENGTH:
162 CTATAAAAGAACAACAACAAATCC 139
                                         5 CAATAAAAGAACAACAACCGATCC 28
                                                                                     21;
                                                                                                         Similarity
                                                                                                                                                                                                                                                                               FastSEQ
                                                                                 Conservative
                                                                                                                                                                                                                                                                               for Windows Version 4.0
                                                                                                       66.2%;
87.5%;
                                                                                 Score 19.2; DB 13; Pred. No. 2e+02; 0; Mismatches 3;
                                                                                                                           Length
                                                                                                                               585;
                                                                                 0;
                                                                                 Gaps
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US-09-560-863-832 US-10-027-632-216183

Sequence

832, App 216183,

0;

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: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-239-676-82
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US-10-239-676-82/c
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-5257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 82, Application US/102
Publication No. US20030082609A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                         SEQ ID NO 82
LENGTH: 9091
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                       Best Local Similarity
                                           Query Match
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     Matches
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                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058 8
DE 10019173 8
DE 10032529 7
DE 10043826 1
                                                                                                                                                                                                              2000-09-01
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-04-06
                                                                                                                                                         TYPE: DNA
                                                                                                                  FEATURE:
                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 945
                                                                                                                                                                                                                                                     2000-06-30
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22; Conserv
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   Conservative
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ilarity 81.5%;
Conservative
                                                                                                                                                                                                                                                                                                          2001-04-06
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                       64.1%;
Score 18.6; DB 14;
Pred. No. 5.9e+02;
0; Mismatches 4;
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Pred. No. 2.6e+02;
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                                     Length 9091;
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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PRIOR EILING DATE: 2000-07-12
PRIOR BODY
                                                              PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                       PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23 PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 46819
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                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 108827.129
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80.8%;
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Pred. No. 5.9e+02
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FILE REFERENCE: 10867,129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
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; ORGANISM: Human
US-10-027-632-77880
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-46819
                                                                                                                                                           Sequence 77881, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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SOFTWARE: FastSEQ for
SEQ ID NO 77880
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Best Local (
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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APPLICATION NUMBER: US 60/146,002
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21; Conserv
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DATE: 2000-02-24
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Pred. No. 5.9e+02;
Pred. No. 5.9e+02;
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5.9e+02;
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US-10-027-632-314242

Sequence 314242, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827,129

APPLICATION NUMBER: US/10/027,632

RESULT 9

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                                                                           Matches
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Best Local
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SEQ ID NO 314241
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GENERAL INFORMATION
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77881
LENGTH: 508
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-04-20
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER:
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PRIOR FILING DATE: 1999-11-23
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                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 108827
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                                                                                                                                                                                              LENGTH: 508
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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129 TCATTCAAAGAGCAACAAGGGATCCC 154
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                                                                                        Similarity
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21; Conserv
                                TCAATAAAAGAACAACCAACCGATCCC 29
                                                                      Conservative
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                                                                                      62.1%;
80.8%;
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                                                                                                                                                                                                                                                                                                              US 60/156,358
                                                                  Score 18; DB
Pred.'No. 5.9e
0; Mismatches
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Pred. No. 5.9e
0; Mismatches
                                                                                                      DB 13;
                                                                                    .9e+02;
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                                                                                                  Length 508;
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; LENGTH: 508
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-314242
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SEQ ID NO 25
LENGTH: 9246
                                                                               Best
                                                                  Matches
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/10265689 Publication No. US20030119775A1
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Best Local
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CURRENT FILING DATE: 2002-10-08
                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-01-15
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US97/06864 PRIOR FILING DATE: 1997-04-22
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BOUILLAUD, FREDERIC
TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
FILE REFERENCE: 1579-376
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                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/353,645 PRIOR FILING DATE: 1999-07-15
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                                                                                                                                         OTHER INFORMATION: "n" bases may be a,
                                                                                                                                                                          ORGANISM: Murine sp.
                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                             FEATURE:
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APPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
2501 GAGGCAATAAAAAAACAACACCCAAT 2476
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FILING DATE: 2000-04-20
APPLICATION NUMBER: US 60/193,483
FILING DATE: 2000-03-29
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APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
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                  1 GCGTCAATAAAAGAACAACCAACCGAT 26
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                                                                             Similarity
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Similarity 80.8%;
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                                                                Conservative
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                                                                            62.1%;
80.8%;
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                                                                             Score 18; DB 14;
Pred. No. 1e+03;
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Pred. No. 5
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RESULT 11

RESULT 13
US-10-027-632-303956/c
; Sequence 303956, Application US/10027632
; GENERAL INFORMATION:

David G

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US-10-027-632-89343/c
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; LENGTH: 32167
; TYPE: DNA
; ORGANISM: Homo saplens
US-09-764-891-8197
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Best Local Similarity
Matches 19; Conserv
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SEQ ID NO 89343
LENGTH: 567
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: POIMORPHISMS in the Human Genome
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                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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CURRENT FILING DATE: 2002-04-30
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 108827.
                                                                                                                                                                                               TYPE: DNA
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389 AATAAAAGAACAACAACTGCT 369
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                                  AATAAAAGAACAACCAACCGAT 26
                                                                            Conservative
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80.8%;
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                                                                        Score 17.8; D
Pred. No. 7.2e
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Pred. No. 1.3e+03
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CURRENT APPLICATION NUMBER: US/09/560,863
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/132,408
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 1008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 832
LENGTH: 634
TYPE: DNA
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US-09-560-863-832/c
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: SEO ID NO 303956
: LENGTH: 567
: TYPE: DNA
: ORGANISM: Human
US-10-027-632-303956
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Best Local 9
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Best Local :
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Patent No. US20020110809A1
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                                                                                                                                      ORGANISM: homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(634)
OTHER INFORMATION: n = A,T,C or G
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PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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                               8 TAAAAGAACAACCGATCCC 29
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TAAAAGAAAAAAACCGATCNC 537
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CATION NUMBER: US 60/156,358
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Zambrowicz, Brian
Sands, Arthur T.
                                                               Conservative
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7-12
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Pred. No. 7.46
0; Mismatches
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Pred. No. 7.2e+02
0; Mismatches
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                                                              Indels
                                                                                            Length 634;
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RESULT 15

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; LOCATION: (1)...(655)
; OTHER INFORMATION: n - A,T,C or
US-10-027-632-216183
Search completed: August
Job time: 115.375 secs
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Best Local :
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SEQ ID NO 216183
                                                                                                                                                Matches
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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FEATURE:
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352 AATTAAAGAACAACAACAGAT 372
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PLICATION NUMBER: US 60/146,002
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19; Conserv
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PLICATION NUMBER: US 60/156,358
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3ER: US_60/218,006
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Pred. No. 7
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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    nucleic search, using sw model

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Match
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Candida sp. rRNA/r
Probe CalA1037 for
Candida species 18
Candida species 18
C. tropicalis 16S
C. albicans 16S rR
C. parapsilosis 16
Probe CalA1038 for
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64.1	64.1	64.1	64.1	٠	64.8	•	•	•	•	•	•	•	•	•	•	•	67.6	•	•	•	•	'n	68.3	•	68.3		69.0		•			72.4	72.4	12.4	;
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syst	n chemically	ide t	Oligonucleotide fo	immune syst	Human chemically m	Haematopoietic cel	phila		DNA to infer yeast	Arabidopsis thalia	Human immune syste	Oligonucleotide fo	Oligonucleotide fo	Drosophila melanog	phila	immune syst	chemicall	Tumour suppressor	Drosophila melanog	Oligonucleotide fo	Oligonucleotide fo	5	Flax rust resistan	cans	Candida albicans e	168	Oligonucleotide fo	Oligonucleotide fo	1de	de	n prostate	haromyces c	z	x iguus	

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## ALIGNMENTS

RESULT 1 AAC81651

Candida sp. rRNA/rDNA hybridisation probe, SEQ

ID NO:55

09-MAR-2001 (first entry)

AAC81651;

AAC81651 standard; DNA;

29 BP

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(GENP-) GEN-PROBE INC.		03-MAY-1999; 99US-0132411.	03-MAY-2000; 2000WO-USI242I.		09-NOV-2000.		WO200066789-A2.		Candida parapsilosis.	Candida viswanathii.	Candida dubliniensis.	Candida tropicalis.	Candida albicans.		nucleic acid matrix; nucleotide array; hybridisation probe; ss.	bacterium; fungus; infection; clinical sample; diagnosis;	Ribosomal nucleic acid; rRNA; rDNA; microorganism identification;

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RESULT 2
AAI70909
ID AAI7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         order address. Likewise, the intermediate order address hybridises ribosomal nucleic acids from a subset of organisms having ribosomal nucleic acids that hybridise at the higher order address. The method and nucleic acid matrix of the invention is used for identifying microorganisms, especially in clinical samples. The method can detect and resolve the identities of microorganisms that are present in a mixed sample. The system is suited to automated analysis, and enables the identification of a disease-causing microorganism without the need for experienced technicians. The present sequence represents a ribosomal nucleic acid-specific hybridisation probe for use in a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biological sample. Probes in the matrix are selected to distinguish between organisms that differ from each other by a known phylogenetic relationship. The addresses include a higher order address (the least organism-specific address which is able to bind to a ribosomal nucleic acid from a broad class of organisms e.g., one common to all fungi), an intermediate address and a lower order address (the most organism-specific). The lower order address hybridises rRNA/FDNA from a subset of organisms whose ribosomal nucleic acids hybridise to the intermediate order address the intermediate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A device for hybridizing nucleic acids useful for identifying microorganisms comprises a solid support and several addresses comprising a probe, disposed on the solid support -
                                                               01-MAY-2000; 2000US-201249P
                                                                                                                                                                                                                                                                                                                     Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                        Candida
                                                                                                                                                                                                                                                                                                                                                                                                                         Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe CalA1037 for Candida species detection and quantitation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29 BP; 13 A; 9 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 40;
                                                                                                                           01-MAY-2001; 2001WO-US13884
                                                                                                                                                                                                                                                         WO200183821-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI70909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI70909 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matrix of the invention.
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(GENP-) GEN-PROBE
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viswanathii;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Candida tropicalis; Candida dubliniensis;
ii; Candida parapsilosis; detection; probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
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Pred. No.
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Query Match
                                                                                                                               from their known phylogenetically nearest neighbours. It is useful for their detection and quantitation. Probe Calal337 is 29 bases in length; has a Tm of 59.5 degree C, and hybridises rRNA in a manner that is enhanced by the presence of helper oligonucleotides (see AA170910-12). The probe is an illustration on oligonucleotide that: (1) hybridises the target nucleic acid unhigh stringency hybridisation conditions; (2) has a length of up to 100 nucleotide bases; and (3) includes at least 15 contiguous nucleotides falling within the sequence given in AA170915 or its
                                                                                                                                                                                                                                                                                                      The present sequence is that of oligonucleotide probe Calal037, which is complementary to a unique segment (see AAT70916) of the 185 ribosomal RNA of Candida albbicans, Candida tropicalis, Candida dubliniensis, Candida viswanathii and Candida tropicalis. The probe is highly specific, and can distinguish these Candida species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel oligonucleotide sequences that are fully complementary to ribosomal RNA or DNA of Candida species, useful for detecting presence of C.albicans, C.dubliniensis, C.viswanathii, C.parapsilosis in test
                                                            Sequence
                                                                                                complement.
acridinium
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hogan JJ,
     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-066537/09.
                                                                                                                                                                                                                                                                                                                                                                                                                        2; Page 19; 33pp; English
     Similarity
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                                                                                                  ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gordon PC;
                                                          BP; 13 A; 9 C; 4 G; 3 T; 0 other;
                                                                                                                  It may include a detectable moiety, such as
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F
                                                                                                  a radioisotope.
100.0%;
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                       DB 24;
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RESULT 3
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                                                                                      01-MAY-2000; 2000US-201249P
                                                                                                                                                                      Candida albicans; Candida tropicalis; Candida dubliniensis; Candida viswanathii; Candida parapsilosis; detection; probe;
                                                      Hogan JJ,
                                                                                                      01-MAY-2001; 2001WO-US13884
                                                                                                                       08-NOV-2001
                                                                                                                                       WO200183821-A2
                                                                                                                                                        Candida albicans
                                                                                                                                                                                               Candida species 18S ribosomal DNA probe domain
                                                                                                                                                                                                                 12-MAR-2002
                                                                                                                                                                                                                                 AAI70915
                                                                                                                                                                                                                                                 AAI70915 standard; DNA; 113
                                                                      (GENP-) GEN-PROBE INC
                                      2002-066537/09.
                                                                                                                                                                                                                                                                                                 1 GCGTCAATAAAAGAACAACAACCGATCCC 29
                                                                                                                                                                                                                                                                                          GCGTCAATAAAAGAACAACAACCGATCCC
                                                       Gordon PC
                                                                                                                                                                                                                 (first entry)
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Novel oligonucleotide sequences that are fully complementary to ribosomal RNA or DNA of Candida species, useful for detecting plof C.albicans, C.dubliniensis, C.viswanathii, C.parapsilosis in

presence

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RESULT 4
AAI70916;
ID AAI70916 standard; r)
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AC AAI70916;
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AC AAI70916;
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DT 12-MAR-2002 (first of the condition of the 
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                                                                                                                                                                                    Claimed hybridisation probes and helper oligonucleotides (see AAI70909-14) correspond to a portion of this sequence or its complement. The probes are highly specific, and can distinguish these Candida species from their known phylogenetically nearest neighbours. They are useful for detection and quantitation.
                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of a unique segment of the 18s ribosomal RNA of Candida albicans, Candida tropicalis, Candida dubliniensis, Candida viswanathii and Candida tropicalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel oligonucleotide sequences that are fully complementary to ribosomal RNA or DNA of Candida species, useful for detecting presence of C.albicans, C.dubliniensis, C.viswanathii, C.parapsilosis in test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segment (see AAI70916) of the 18S ribosomal RNA of Candida albicans, Candida tropicalis, Candida dubliniensis, Candida viswanathii and Candida tropicalis. Claimed hybridisation probes and helper oligonucleotides (see AAI70909-14) correspond to a portion of this sequence or its complement. The probes are highly specific, and can distinguish these Candida species from their known phylogenetically and candida tropically specific and candidation of the probes are supplied to the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000; 2000US-201249P.
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    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viswanathii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      species 18S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neighbours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGTCAATAAAAGAACAACCAACCGATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gordon PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US13884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida tropicalis; Candida dubliniensis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33pp; English
                                                                                                                  A; 23 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33pp; English.
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida parapsilosis; detection; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        They are useful for detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                              27 G; 35 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 G;
    Pred. No.
                                    Score 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA probe domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB 24
Pred. No. 0.034;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
0.034;
                            DB 24;
                                                                                                                  0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                            Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and quantitation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Conservative

0

Mismatches

0

0,

Gaps

0,

RESULT 6 AAH21230/c ID AAH21230 standard;

DNA;

431

ВP

밁 Ş

408  $\vdash$ 

GCGTCAATAAAAGAACAACAACCGATCCC

Conservative

0

Indels

0

Gaps

0;

GCGTCAATAAAAGAACAACAACCGATCCC

380 29

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RESULT 5
AAH21229/c
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  Matches
                          Query Match
                                                                                              This invention describes a novel method for detecting microbial DNA/RNA (I) by concentrating (I) from a sample, adding at least one labeled oligonucleotide (ON), performing temperature-dependent hybridization and determining (I) from the physical properties of the (I)-ON complex, e.g. the temperature dependence of hybridization. The method is used for rapid determination of microbial genomic RNA or DNA, particularly for diagnosis of bacterial infections (e.g. sepsis) or fungal infections (particularly in intensive care patients), also for monitoring food and water, and for veterinary or forensic investigations. The method provides quick retermination/identification of microbial nucleic acid. It is very sensitive, allowing early diagnosis of infection. AAH21160-AAH21231
                                                 Sequence
                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                          Rapid determination of microbial nudiagnosing bacterial infections, by hybridization with oligonucleotides
                                                                                                                                                                                                                                                                                                                                              WPI; 2001-425677/45
                                                                                                                                                                                                                                                                                                                                                                      Hoeft A,
                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999;
31-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida tropiealis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH21229
                                                                                     represent primers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-DEC-2000; 2000WO-DE04610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200148237-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hybridization; diagnosis; bacterial food monitoring; water monitoring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH21229;
                                                                                                                                                                                                                                                                                                                                                                                               (STUE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                            (HOEF/)
               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
 29;
                                                                                                                                                                                                                                                                                                                                                                                              HOEFT A.
STUEBER F.
             Similarity
                                                   429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA; 429
                                                                                                                                                                                                                                                                                                                                                                      Stueber F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGTCAATAAAAGAACAACAACCGATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGTCAATAAAAGAACAACCAACCGATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS
                                                                                                                                                                                                                                                                   Figure 13; 57pp;
                                                   BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                    2000DE-1027113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16S rRNA DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                               99DE-1062895
                                                 114 A;
           100.0%;
                                                                                       probes used to illustrate the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monitoring; veterinary;
                                                   85 C;
 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВÞ
                                                                                                                                                                                                                                                                   German.
Pred. No. 0.
; Mismatches
                                                   109
                        Score 29;
                                                                                                                                                                                                                                                                                                      nucleic acid, useful e.g. for by analysis of temperature-dependent
                                                G; 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSASRSUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
                                                Τ,
                          В
             .037;
                      22;
                                                2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sepsis; fungal infection;
forensic; primer; probe;
                      Length 429;
                                                                                      of the
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RESULT 7
AAH21228/c
ID AAH212
XX
AC AAH212
XX
DT 13-SEP
XX
DE C. par
XX
KW Hybrid
KW food m
                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel method for detecting microbial DNA/RNA (I) by concentrating (I) from a sample, adding at least one labeled oligonucleotide (ON), performing temperature-dependent hybridization and determining (I) from the physical properties of the (I)-ON complex, e.g. the temperature dependence of hybridization. The method is used for rapid determination of microbial genomic RNA or DNA, particularly for diagnosis of bacterial infections (e.g. sepsis) or fungal infections (particularly in intensive care patients), also for monitoring food and water, and for reterinary or forensic investigations. The method provides quick (typically less than 3 hours) quantitative and qualitative determination/identification of microbial nucleic acid. It is very sensitive, allowing early diagnosis of infection. AAH21160-AAH21231 represent primers and probes used to illustrate the method of the
 Hybridization; diagnosis;
food monitoring; water mor
                                          C. parapsilosis 16S rRNA DNA fragment YSASRSUF
                                                                                                    AAH21228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Figure 13; 57pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rapid determination of microbial nucleic acid, udiagnosing bacterial infections, by analysis of hybridization with oligonucleotides
                                                                        13-SEP-2001
                                                                                                                                AAH21228 standard; DNA; 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-425677/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1999; 99DE-1062895
31-MAY-2000; 2000DE-1027113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200148237-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybridization; diagnosis; bacterial infection; food monitoring; water monitoring; veterinary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoeft A, Stueber F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STUE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOEF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-DEC-2000; 2000WO-DE04610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH21230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                albicans 16S rRNA DNA fragment YSASRSUA
                                                                                                                                                                                                      410
                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) HOEFT A.
) STUEBER F.
                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                   431
                                                                                                                                                                                                    GCGTCAATAAAAGAACAACAACGATCCC
                                                                                                                                                                                                                               GCGTCAATAAAAGAACAACAACCGATCCC 29
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                  ВP;
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                  115 A; 86
                                                                                                                                                                                                                                                                        100.0%;
monitoring;
bacterial infection;
nitoring; veterinary;
                                                                                                                                                                                                                                                                                                                   Ç
                                                                                                                               ВP
                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                       Score 29;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                  110 G;
                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                  120 T; 0 other;
                                                                                                                                                                                                    382
                                                                                                                                                                                                                                                                        DB 22;
0.037;
                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful
sepsis; fungal infection
forensic; primer; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sepsis; fungal infection;
forensic; primer; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful e.g. for
temperature-dependent
                                                                                                                                                                                                                                                                                    Length 431;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                           0,
             infection;
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                           0
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Query Match
Best Local
                                                                                            Matches
                                                                                                                                                                                                                                              (I) by concentrating (I) from a sample, adding at least one labeled oligonucleotide (ON), performing temperature-dependent hybridization and determining (I) from the physical properties of the (I)-ON complex, e.g. the temperature dependence of hybridization. The method is used for rapid determination of microbial genomic RNA or DNA, particularly for diagnosis of bacterial infections (e.g. sepsis) or fungal infections (particularly in intensive care patients), also for monitoring food and water, and for veterinary or forensic investigations. The method provides quick (typically less than 3 hours) quantitative and qualitative determination/identification of microbial nucleic acid. It is very sensitive, allowing early diagnosis of infection. AAR31160-AAR31231 represent primers and probes used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HOEF/)
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rapid determination of microbial nucleic acid, useful e.g. for diagnosing bacterial infections, by analysis of temperature-dependent hybridization with oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-425677/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-1999; 99DE-1062895; 31-MAY-2000; 2000DE-1027113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida parapsilosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200148237-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes a novel method for detecting microbial DNA/RNA
                                                                                         Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOEFT A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STUEBER F.
GCGTCAATAAAAGAACAACAACCGATCCC
                                         GCGTCAATAAAAGAACAACCAACCGATCCC 29
                                                                                                                                                                                   432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Figure 13;
                                                                                         Conservative
                                                                                                                                                                                   BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-DE04610
                                                                                                                                                                                      114
                                                                                                             100.0%;
                                                                                                                                                                                 A; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57pp;
                                                                                                                                                                                   ü
                                                                                         0;
                                                                                       Score 29; DE
Pred. No. 0.0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        German.
                                                                                                                                                                                      110
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                                                                                                                                                                                   121
                                                                                                               0.037;
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                                                                                                                                                                                   T; 1 other;
                                                                                                                                     22;
                                                                                         0
                                                                                                                                     Length 432;
                                                                                       0
                                                                                       Gaps
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RESULT 8
AAI70913
                       08-NOV-2001
                                      WO200183821
                                                       Candida albicans
                                                                       Candida
                                                                              Candida
                                                                                             Probe CalA1038 for Candida species detection and
                                                                                                                12-MAR-2002
                                                                                                                                               AAI70913 standard; DNA; 28.
                                                                     albicans; Ca
viswanathii;
                                                                                                              (first entry)
                                                                    Candida tropicalis; Candida dubliniensis;
ii; Candida parapsilosis; detection; probe
                                                                                             quantitation
                                                                      88
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01-MAY-2001; 2001WO-US13884

В S

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of oligonucleotide probe CalAlO38, which is complementary to a unique segment (see AAI70916) of the 185 ribosomal RNA of Candida albicans, Candida tropicalis, Candida Candida tropicalis, Candida Candida tropicalis, Candida Candida tropicalis, Candida Candida tropicalis, The 20 probe is highly specific, and can distinguish these Candida species CC useful for their detection and quantitation. Hybridisation to rRNA CC is enhanced by the presence of helper oligonucleotides, e.g. the Tm CC is enhanced by the presence of helper oligonucleotides, e.g. the Tm CC is enhanced by the presence of helper oligonucleotides, e.g. the Tm CC (see AAI70914) and CalAlO66 (see AAI70912). The probe is an CC illustration of an oligonucleotide that: (1) hybridises the target CC instance acid under high stringency hybridisation conditions; (2) CC least 15 contiguous nucleotides bases; and (3) includes at CC least 15 contiguous nucleotides falling within the sequence given CC such as an acridinium ester or a radioisotope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 26; 33pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel oligonucleotide sequences that are fully complementary to ribosomal RNA or DNA of Candida species, useful for detecting presence of C.albicans, C.dubliniensis, C.viswanathii, C.parapsilosis in test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-066537/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000; 2000US-201249P
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
                                                                                                                                                                                                                    non-lactate-assimilating; yeast; silage; aerobic stability;
r recovery; spoilage; animal feed; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gordon PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 13 A; 8 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.6%;
                                          Ruser BG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                          Hoganson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ນ.077;
0;
                                          DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 10
AAF23018/c
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Best Local
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                                                                                          24-NOV-1987;
11-DEC-1991;
24-NOV-1986;
07-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spoilage organisms, by adding the yeast strain to feed, preferably upon ensiling and/or by maintaining the silage for 30 days or more. Also, a strains of S. exiguus which do not assimilate lactate and which inhibit growth of other yeast strains associated with the spoilage of silage. Also, an isolated yeast strain having a characteristic rRNA sequence or sequence that can be hybridized to it, which can also inhibit growth of assimilate lactate. The process is useful for improving aerobic stability, by increasing dry matter recovery by reducing aerobic spoilage. The inoculant is safe and nonhazardous as an additive
                                    McDonough SH,
                                                                                                                                                  22-FEB-1994;
24-NOV-1987;
                                                                                                                                                                                                                       21-NOV-2000
                                                                                                                                                                                                                                                                          Saccharomyces
                                                                                                                                                                                                                                                                                                               Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrheae;
                                                                                                                                                                                                                                                                                                                               Probe; PCR primer; 5s rRNA; 16s rRNA; 23s rRNA; 28s rRNA; Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. col
                                                                (GENP-) GEN-PROBE INC
                                                                                                                                                                                             30-MAY-1995;
                                                                                                                                                                                                                                                   US6150517-A.
                                                                                                                                                                                                                                                                                                         bacterium;
                                                                                                                                                                                                                                                                                                                                                                              Yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention for use as a silage inoculant, comprises yeast strain SE24, SE136 or SE151, having ATCC accession numbers 74441, 74442 or 74443 respectively, and optionally comprise their derivatives or mutants. The composition optionally comprises a carrier. The invention also describes a method for treating animal feed or silage susceptible to growth of
                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF23018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF23018 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1776 BP; 474 A; 343 C; 453 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-lactate-assimilating yeast for improving the aerobic stability silage, by inhibiting the growth of yeast strains associated with spoilage, using a strain of Saccharomyces exiguus as inoculant -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel yeast strain useful as an inoculant for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; Fig 3; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                improving aerobic stability, by increasing reducing aerobic spoilage. The composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1067
                                                                                                                                                                                                                                                                                                                                                                          18S rRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCGTCAATAAAAGAACAACAACCGATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTCATTAAAAAAACACCACCCGATCCC
                                                                                                                                                                                                                                                                                                         SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                          87WO-US03009.
91US-0806929.
86US-0934244.
87US-0083542.
                                    Kop JA,
                                                                                                                                                                                                                                                                            cerevisiae
                                                                                                                                                 94US-0200866.
87US-0295208.
                                                                                                                                                                                           95US-0454063
                                                                                                                                                                                                                                                                                                                                                                                                                                                               rRNA; 1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                   Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21;
                                   RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by increasing dry matter recovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                   Hogan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                   JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                             188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                              Legionella;
                                                                                                                                                                                                                                                                                                                                              rRNA;
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0,

WPI; 2001-060029/07

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RESULT 11
ABA99033
ID ABA99033
ID ABA99033
ID ABA9903X
XX ABA990
XX ABA99
XX Sacch
XX Eco2.
KW Fibre
KW Guall
XX Sacch
XX Guall
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eco2.0; tree lineage; fibre length; wood density; fibre collapsibility; fibre coarseness; growth rate; cell wall thickness; lignin content; gualacyl lignin content; syringyl lignin content; carbohydrate content; kraft pulp yield; mechanical pulp energy demand; chemical pulping; fibre quality; wood quality; YLR154c; ds.
                                                                                                                                                                                                Identifying tree lineage for identifying trees having superior phenotype, e.g. fibre length, comprises hybridizing a DNA probe to tygenomic DNA isolated from spruce live tissue and assessing intensity the hybridization pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli, Mycobacteria, Myco
Legionella, Salmonella,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preparing a probe for nucleic acid hybridization assays comprises constructing a nucleotide polymer sufficiently complementary to hybridize to an rRNA region that distinguishes non-viral target from non-viral non-target species -
            phenotypes.
                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                      Potter
                                                                                                                                                                                                                                                                                                                                                                                                                 (PPCA ) PULP & PAPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200204663-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            АВА99033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA99033 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
sequence represents a fragment of Saccharomyces cerevisiae chromosome cosmid reading frame ORF YLR154c, including the complete sequence of ECO2.0 probe. The invention relates to a novel method for identifying e lineage capable of expressing desired biological and/or biochemical notypes. The method is useful for identifying trees having superior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1067
                                                                                                                                                                                                                                                                                                                     2002-179711/23.
                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1802
                                                                                                                                                                                                                                                                                                                                                                   Watson
                                                                                                                                               Fig 4; 48pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention provides novel methods of producing probes for thitication of a number of microorganisms. These include acteria, Mycoplasma, Campylobacter, Chlamydia, Enterobac Salmonella, Pseudomonas, Neisseria gonorrheae, fungi an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-213585P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-CA00927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
878..10537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                   PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 A; 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 3420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.48; 82.88;
                                                                                                                                                                                                                                                                                                                                                                                                                 RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Eco2.0 probe complete sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                 INST
                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                               CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XII cosmid reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ģ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fungi and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLR154c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                   tree
ty of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use
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cancer in a patient;
(d) assessing the eff
in a patient;
(e) selecting a compo
(f) assessing the pro

composition omposition for prostate cell

carcinogenic

prostate cancer in a patie c potential of a compound; inhibiting prostate cancer

patient;

efficacy

of a

therapy for inhibiting

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8888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 24
                                                     The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phenotype, including fibre length, wood density, fibre collapsibilit fibre coarseness, cell wall thickness, growth rate, lignin content, guaiacyl lignin content, syringyl lignin content, carbohydrate context kraft pulp yield, mechanical pulp energy demand, chemical uptake for chemical pulping, extractive content and extractive compounds. The tinclude trees of the genus Pichia, Populus, Betula, Abies, Larix, Te Ulmus, Prunus, Quercus, Malus, Arbutus, Salix, Platanus, Accer, Tsuge Pseudotsuga, Pinus, Fraxinus, Eucalyptus, Acacia, Abrus, Cupressus, Fagus, Juniperus, Thuja and Canya. The Eco2.0 probe is useful for predicting wood or fibre quality.
                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer stage of prostate cancer \,
                                                                                                                                              Claim 1; Page 9808; 11750pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                      09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                   16-MAR-2000;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABV50391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV50391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                        (MILL-)
                                                                                                                                                                                                                                                                                                                                                          17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2001;
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2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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CC This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'.CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the CC lasses of oligomers, the degree of methylation is calculated. The method CC is used: (1) for diagnosis and/or prognosis of side effects of CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory CC systems etc., particularly by detecting mutations or single nucleotide CC types and for investigating cell differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously.

CC method for determining the degree of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12;
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05-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-2002
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Pred. No. 1
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em; cardiovascular
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This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one CC member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the CC classes of oligoners, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of CC classes of oligoners, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of CC chasses of oligoners, the degree of diseases, e.g. cancer, disorders CC of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide CC cybes and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

CC method for determining the degree of cytosine methylation described in the absolute of the invention.
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ID ABQ49
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Best Local :
                                                                                                                                                                                                                                                                                                                                                  Claim 12; 56pp + Sequence Listing; 56pp;
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drug; side effect; cancer; ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide for detecting
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05-SEP-2000;
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                            disclosure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell differentiation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 A; 128
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82.1%;
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single nucleotide
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This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the C label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory cystems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the types and for investigating cell differentiation. The method allows the contral nervous cardiovascular to be determined simultaneously. ABQ1310-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
ABQ22352/c
ID ABQ22352 standard; DNA; 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -
                                                       Sequence 1080 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; dlagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-371829/40.
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide for detecting cytosine methylation SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG
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                                                     152 A; 124 C; 382 G; 418 T; 4 other;
   69.0%;
82.1%;
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996 CGATAAAAAAAAAAACAACACCCGATCCC
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         2 CGTCAATAAAAGAACAACAACCGATCCC 29
                                       Conservative
                                     Mismatches
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                                     Indels
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                                     Gaps
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Search completed: August Job time : 182.25 secs 6, 2003, 23:02:39

Minimum DB :

length: length:

20000000000

Total number

of.

2888711 seqs, 20454813386 residues hits satisfying chosen parameters:

5777422

Database

GenEmbl: \*

gb\_ba:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Title: Perfect score: Sequence:

> US-09-846-797-1 29

gcgtcaataaaagaacaacaaccgatccc

29

OM nucleic - Run on:

nucleic search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen

Ltd.

August 6, 2003, 21:26:11 ; Search time 710.047 Seconds (without alignments) 1670.846 Million cell updates/sec

Scoring table:

IDENTITY\_NUC Gapext 1.0

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Pred. No. 1s the number of results predicted by chance to have a
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REFERENCE AUTHORS TITLE RESULT 1
AX045494
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
KEYWORDS
SOURCE
ORGANISM Result No. 00000000000000000 000000000000000000000 JOURNAL Score Sequence 55 AX045494 AX045494.1 Hogan, J.J.

Polynucleotide matrix-based method of identifying microorganisms Patent: WO 0066789-A 55 09-NOV-2000;

Gen-Probe Incorporated (US) synthetic construct synthetic construct artificial sequences. 100.00 1100.00 Query 100.0 Match 55 Length 28 741 1747 1753 1773 1773 1773 1020 1020 1043 1363 1363 17717 17717 1738 1738 1738 GI:11343957 29 bp from Patent WO0066789. AB054292 LECBS18SR AB013529 AB013560 AB030914 AB030913 CXU63036 AY249514 AY227020 AY227021 AB105434 YSASRSUG YSASRSUF AB013533 AB013549 AB013589 AF114470 AY227019 CAAJ5123 AB013586 AB013588 AY055856 AY055855 YSASRSUH ALIGNMENTS SUMMARIES DNA AX298063 Sequence
AX298086 Candida t
AND54292 Pichia sp
X78600 L. elongispo
X78600 L. elongispo
AND13529 Candida s
AND3540 Candida s
AND3540 Candida s
AND3914 Debaryomy
AND3914 Pichia gu
AY227020 Pichia gu
AY227021 Pichia fa
AND6444 Pichia fa
AND64440 Pichia st
AND64480 Pichia st AF247474 Unidentif
AB030915 Candida p
AF114470 Candida p
AF114470 Candida p
AF227019 Candida p
AJ005123 Candida n
AG0309 C. LTOpLCali
M60309 C. LTOpLCali
M60307 C. parapsilo
AB013533 Candida s
AB013549 Candida s
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AF013548 Candida p
AF013548 Candida p
AF055855 Candida p
AY055855 Candida p
AY055855 Candida p
AY055857 Candida p
AY055857 Candida p
AY055857 Candida p
AF06302 C.albicans
AR063785 Sequence
E15168 Candida alb
X53497 Candida alb Description PAT Candida s Candida z Sequence Sequence Sequence Sequence 24 -NOV-2000

gb\_pat:\* em\_pat:\*
em\_ph:\* gb\_sy:\* gb\_un:\* gb\_v1:\* 4: 40\_qb em\_htg\_inv:\*
em\_htg\_other:\* em\_un: em\_mu:\*
em\_om:\* gb\_pr:\* 4: Td\_q gb\_om:\* em\_htgo\_mus:\*
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                                                                                              Candida albicans
Eukaryota; Fungi; !
Saccharomycetales;
                                                                                                                                                                  Sequence 7 from AX298065
                                                                                                                                                                                                                                          Candida albicans
Eukaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                              Hogan, J.J. and Gordon, P.C. Polynucleotide probes for detection
                                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 bp
Sequence 1 from Patent WO0183821
AX298059
                                          Patent: WO 0183821-A 7 08-NOV-2001;
                                                       species
                                                                                                                                 Candida albicans
                                                                                                                                                        AX298065.1
                                                                                                                                                                                        AX298065
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gen-Probe
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                   Location/Qualifiers
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∕organism="Candida albicans"
                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:5476"
9 c 4 g
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/mol_type="genomic DNA"
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                        GI:17128151
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100.0%; Pred. No.
tive 0; Mismatch
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Patent WO0183821
                                                                                               Ascomycota; Saccharomycotina; mitosporic Saccharomycetales;
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saccharomcyete isolate SPT1
saccharomcyete isolate SPT1
Eukaryota; Fungi; Ascomycota;
unclassified Saccharomycetes.
 2 (bases 1 to 510)
Trosok,S.P., Driscoll,B.T.
                                                                      1 (bases 1 to 510)
Trosok, S.P., Luong, J.H., Juck, D.F. and Driscoll, B.T. Characterization of two novel yeast strains used in biosensors for wastewater
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Unidentified saccharomycetalean
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Polynucleotide probes for detection
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Saccharomycetales; mitosporic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Candida albicans"
/mol_type="mRNA"
/db_xref="taxon:5476"
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27 c 23 g
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/db_xref="taxon:5476"
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Candida a
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.

1 (bases 1 to 1029)

Shintani,T. and Matsumoto,Y:
Candida parapyllosis gene for 185 rRNA, partial sequence
Published Only in DataBase (1999)

2 (bases 1 to 1029)

Shintani,T. and Matsumoto,Y.
Direct Submission
Submitted (10-AUG-1999) Tomoyoshi Shintani, Industrial Research
Center of Ehime Prefecture, Laboratory of Food Process; 487-2
                                                                                                                                                                                                                                                                                                                                                                       Center of Ehime Prefecture, Laboratory of Food Process; 487-2 Kumekubota, Matsuyama, Ehime 791-1101, Japan (E-mail:shintani@iri.pref.ehime.jp, URL:www.iri.pref.ehime.jp, Tel:81-89-976-7612, Fax:81-89-976-7313)
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Candida parapsilosis gene for
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Submitted (20-MAR-2000) Natural Resource Sciences, McGill University, 21,111 Lakeshore Rd., Ste-Anne-de-Bellevue, P
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Candida parapsilosis
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albicans 18S ribosomal F
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/mol_type="genomic DNA"
/strain="IEY2"
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195 c 249 g 294 t
                                                                                                                                                                                                                                                                                /db_xref="taxon:5480"
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87 c 126 g 158 t
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/mol_type-"genomic DNA"
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/note="isolated from pulp mill ef
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AY227019
                                                                                                                                                             Submitted (29-JAN-2003) Molecular Hokkaido University, North 9 West
                                                                                                                                                                                                       Sujaya, I.N., Tamura, Y., Kikushima, N., Yata, H.,
                                                                                                                                                                                                                                           Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                           Sujaya,I.N., Tamura,Y., Tanaka,T., Yamaki,T., Ikeda,T., Kikushima,N., Yata,H., Yokota,A., Asano,K. and Tomita,F. Molecular monitoring of Zygosaccharomyces rouxii strain
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Morris,M.L., Andrews,R.H., Rogers,A.H. and Ellis,D.H.
18S rRNA gene full sequence for the type strain of Candida albicans, CBS 562
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AF114470.1
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/strain="CCO 3"
/db_xref="taxon:5480"
<1. .>1670
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328 c 432 g 461 t
                                                                                      /organism="Candida parapsilosis"
/mol_type="genomic DNA"
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319 c 427 g 452 t
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/mol_type="genomic DNA"
/strain="CBS 562"
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                                                                                                                                                            Bioscience,
9, Sapporo,
                                                                                                                                                                                                         Asano, K.
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                                                                                                                                                            Sapporo, Hokkaido 0608589,
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CAAJ5123/c
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                                                                            Candida viswanathii
Candida viswanathii
Eukaryota; Fungi; Ascomycota; S:
Saccharomycetales; mitosporic S:
1 (bases 1 to 1723)
Barns, S. M., Lane, D. J., Sogin, M.
                                                                                                                                                                                                                                                                              985
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C.viswanathii small subunit ribosomal RNA
M60309
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Candida albicans SSU rRNA gen
AJ005123
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kerkmann,M.L., Schuppler,M., Paul,K.D., Schoenian,G. and Smith,M.T. Red-pigmented Candida albicans in patients with cystic fibrosis J. Clin. Microbiol. 37 (1), 278 (1999)
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Candida albicans
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                              J. Bacteriol, 173
91177814
                                                                  Evolutionary relationships
                                                                                                                                                                          M60309.1
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Schuppler, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Clin. Microbiol. 99138628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             small subunit ribosomal RNA; SSU
                                                         relatives
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<1. .>1700
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/product="small subunit ribosomal 328 c 443 g 471 t ]
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/mol_type="genomic DNA"
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Pred No. 0.
                                          2250-2255 (1991)
                                                                                Sogin, M.L.,
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Saccharomycetales;
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                                                                 pathogenic Candida species an
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                          AUTHORS
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                     Candida parapsilosis
Candida parapsilosis
Eukaryota; Fungl; Ascomycota; Saccha
Saccharomycetales; mitosporic Saccha
1 (bases 1 to 1739)
Barns, S.M., Lane, D.J., Sogin, M.L., B
Evolutionary relationships among pat
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                                                                                                                                           C.parapsilosis small subunit M60307
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1 (bases 1 to 1736)
B1 (bases 1 to 1736)
B2 (bases 1 to 1736)
B3 (bases 1 to 1736)
B4 (bases 1 to 1736)
B5 (bases 1 to 1736)
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/mol_type="TRNA"
/db_xref="taxon:5482"
/tissue_lib="ATCC 750"
1 1736
                                                                                                                                                                                                                                                                                                                                                /product="small subunit ribosomal RNA" 320 c 411 g 465 t 100 oth
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/mol_type="rRNA"
/db_xref="taxon:5486"
/tissue_lib="arcc 22891"
                                                                                                                               GI:176366
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173 (7),
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2250-2255 (1991)
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Pred. No. 0.
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ribosomal RNA
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                        pathogenic
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                                    Bibeau, C.
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                      . and Weisburg, W.G. Candida species ar
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and Weisburg, W.G.

PLN 12-FEB-2001

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species

and

Saccharomycetes; ; Candida.

PLN 12-FEB-2001

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Gaps

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RESULT 14
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ABO13549
Candida s
ABO13549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida viswanathii
Candida viswanathii
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Eukaryota; Fungi; Mitosporic Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                           Submitted (30-APR-1998) Takashi Sugita, The Institute of Physical and Chemical Research (RIKEN), Japan Collection of Microorganisms (JCM); 2-1 Hirosawa, Wako, Saitama 351-0198, Japan (E-mail:sugita@my-pharm.ac.jp, Tel:81-48-462-1111(ex.5135), Fax:81-48-462-4619)
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/mol_type="genomic DNA"
/strain="JCM 1601"
/db_xref="taxon:5486"
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338 c 454 g 494 t
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/tissue_lib="ATCC 22019"
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AUTHORS
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Submitted (30-APR-1998) Takashi Sugita, The Institute of Physical and Chemical Research (RIKEN), Japan Collection of Microorganisms (JCM); 2-1 Hirosawa, Wako, Saitama 351-0198, Japan (E-mail:sugita@my-pharm.ac.jp, Tel:81-48-462-1111(ex.5135), Fax:81-48-462-4619)
                                                                                                                                                                                                                                                                     Non-universal usage of the leucine CUG codon phylogeny of the genus Candida Syst. Appl. Microbiol. 22 (1), 79-86 (1999) 99204096
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Syst. Appl. Microbiol. 22 (1), 79-86 (1999)
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Similarity 100.0%;
29; Conservative (
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Fax:81-48-462-4619)
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